

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:28:57 ; Search time 11.2727 Seconds  
(without alignments)  
102.373 Million cell updates/sec

Title: US-09-743-225-8.

Perfect score: 58

Sequence: 1 NTLKTPRVGGXA 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR76:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	67.2	443	2 F69022	methyl coenzyme M
2	39	67.2	443	2 A28544	methyl coenzyme M
3	38	65.5	991	2 S57385	probable membrane
4	37	63.8	704	1 DJBPT7	DNA-directed DNA p
5	36	62.1	257	2 G86767	N-acetylglucosamin
6	36	62.1	266	2 H86407	F3H9.15 protein -
7	36	62.1	451	2 A64310	methyl coenzyme M
8	35	60.3	235	2 E90553	hypothetical prote
9	35	60.3	235	2 E85504	hypothetical prote
10	35	60.3	235	2 C64744	yaeb protein - Esc
11	35	60.3	235	2 AG0532	conserved hypothet
12	35	60.3	333	2 T34260	hypothetical prote
13	35	60.3	333	2 F83783	tartrate dehydroge
14	35	60.3	357	2 H70346	undecaprenyl-phosp
15	35	60.3	410	1 DEECPG	phosphoglycerate d
16	35	60.3	410	2 D85947	D-3-phosphoglycera
17	35	60.3	410	2 H91101	D-3-phosphoglycera
18	35	60.3	413	2 AC0112	phosphoglycerate d
19	35	60.3	514	2 T29552	inward rectifier p
20	35	60.3	2591	2 T30288	pristinamycin I sy
21	34	58.6	352	2 JC2456	inhibin beta-C cha
22	34	58.6	365	2 T04718	hypothetical prote
23	34	58.6	371	1 S49786	3-isopropylmalate
24	34	58.6	377	1 A26499	regulatory protein
25	34	58.6	409	2 C82072	D-3-phosphoglycera
26	34	58.6	441	2 H82642	hypothetical prote
27	34	58.6	446	2 C87130	sugar transport pe
28	34	58.6	644	2 D85359	hypothetical prote
29	34	58.6	742	1 SYB526	phosphoribosylform

30	34	58.6	1090	2 S59077	cellulose 1,4-beta
31	34	58.6	1908	2 T42707	hypothetical prote
32	34	58.6	2329	2 T28125	hypothetical prote
33	33	56.9	169	2 B70233	hypothetical prote
34	33	56.9	198	2 E86183	hypothetical prote
35	33	56.9	239	2 F97542	hypothetical prote
36	33	56.9	263	2 G71114	probable ORF2 prot
37	33	56.9	263	2 E75046	hypothetical prote
38	33	56.9	267	2 F82701	conserved hypothet
39	33	56.9	290	1 H70530	probable extrageni
40	33	56.9	336	2 T41543	probable cell cycl
41	33	56.9	350	1 VGBE63	glycoprotein gp63
42	33	56.9	398	2 T09982	rfe protein - Myco
43	33	56.9	399	2 C87051	probable glycosylt
44	33	56.9	400	2 S64729	protein secretion
45	33	56.9	404	2 B70774	probable rfe prote

## ALIGNMENTS

### RESULT 1

F69022  
methyl coenzyme M reductase (EC 1.8.-.-) I beta chain - Methanobacterium thermoautotroph  
C:Species: Methanobacterium thermoautotrophicum  
A:Variety: strain Delta H  
C:Date: 05-Dec-1997 #sequence\_revision 09-Apr-1999 #text\_change 11-Jun-1999  
C:Accession: F69022; S78580  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T  
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, J.  
S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu  
A:Reference number: A69000; MWID:98037514; PMID:93711463  
A:Accession: F69022  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'MIVRREK', 1-443 <MTH>  
A:Cross-references: GB:AE000885; GB:AE000666; NID:G2622256; PIDN:AAB85657.1; PID:G262  
A:Experimental source: strain Delta H  
A:Note: an incorrect initiation codon was used  
R:Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.  
Eur. J. Biochem. 194, 871-877, 1990  
A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium th  
A:Reference number: S13864; MWID:91099370; PMID:2269306  
A:Accession: S78580  
A:Molecule type: protein  
A:Residues: 2-15 <ROS>  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1168  
A:Complex: heterohexamer of two alpha (see PIR:B69022), two beta and two gamma (see P  
C:Function:  
A:Description: catalyzes the reaction of methyl coenzyme M (2-(methylthio)ethanesulf  
de and methane  
A:Pathway: methanogenesis  
C:Superfamily: methyl coenzyme M reductase beta chain  
C:Keywords: heterohexamer; methanogenesis; oxidoreductase  
F;2-443/Product: methyl coenzyme M reductase I beta chain #status experimental <MAT>  
F;367/Active site: Tyr #status predicted

Query Match 67.2%; Score 39; DB 2; Length 443;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 8; Conservatve 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTLKTPRVGGXA 12  
| | | | |  
Db 55 NALKTKVGGPA 66

### RESULT 2

A28544  
methyl coenzyme M reductase (EC 1.8.-.-) I beta chain - Methanobacterium thermoautotr

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submitted to the Protein Sequence Database, July 1996
A;Reference number: S66775
A;Accession: S66778
A;Molecule type: DNA
A;Residues: 1-991 <DUN>
A;Cross-references: EMBL:Z74826; NID:g1419921; PIDN:CAA99096.1; PID:g1419922; MIPS:YO
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:PHM7
A;Cross-references: SGD:S0005444
A;Map position: 15L
C;Superfamily: yeast probable membrane protein YOL084w
C;Keywords: transmembrane protein
F;14-30/Domain: transmembrane #status predicted <TM1>
F;95-111/Domain: transmembrane #status predicted <TM2>
F;141-157/Domain: transmembrane #status predicted <TM3>
F;392-408/Domain: transmembrane #status predicted <TM4>
F;442-458/Domain: transmembrane #status predicted <TM5>
F;480-496/Domain: transmembrane #status predicted <TM6>
F;585-601/Domain: transmembrane #status predicted <TM7>
F;641-657/Domain: transmembrane #status predicted <TM8>
F;665-681/Domain: transmembrane #status predicted <TM9>

Query Match 65.5%; Score 38; DB 2; Length 991;
Best Local Similarity 77.8%; Pred. NO. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NTLKPRVG 9
Db 569 NTLATPRMG 577
|||||:|

RESULT 4
DJBPT7
DNA-directed DNA polymerase (EC 2.7.7.7) phage chain - phase T7
N;Alternate names: T7 DNA polymerase
C;Species: phage T7
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 11-Jun-1999
C;Accession: A00716; S42311
R;Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94615
A;Accession: A00716
A;Molecule type: DNA
A;Residues: 1-704 <DUN>
R;Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7
A;Reference number: S42283; MUID:83241725; PMID:6864790.
A;Accession: S42311
A;Molecule type: DNA
A;Residues: 1-704 <DUN>
A;Cross-references: EMBL:V01145; NID:g431187; PIDN:CAA24412.1; PID:g15591
C;Comment: T7 DNA polymerase is composed of two chains. One is encoded by the phase 9
each chloroplasts can be substituted for the E. coli subunit and the resultant polymer
C;Comment: In addition to polymerase activity, T7 DNA polymerase exhibits a 3' to 5',
C;Genetics:
A;Gene: 5
A;Map position: 35.94-41.23
C;Superfamily: phage T7 DNA-directed DNA polymerase phage chain
C;Keywords: DNA binding; nucleotidyltransferase

Query Match 63.8%; Score 37; DB 1; Length 704;
Best Local Similarity 75.0%; Pred. NO. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LKTPRVGG 10
Db 289 IKTPKVG 296
|||||:|

RESULT 5
G86767

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N-Acetylglucosamine catabolic protein [imported] - *Lactococcus lactis* subsp. *lactis* (str C; Species: *Lactococcus lactis* subsp. *lactis*  
C; Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C; Accession: G86767  
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mairame, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A; Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s  
A; Reference number: A86625; MIM:21235186; PMID:11337471  
A; Accession: G86767  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-257 <STO>  
A; Cross-references: GB:AE005176; PID:g12724105; PIDN:AAK05241.1; GSPDB:GN00146  
A; Experimental source: strain IL1403  
C; Genetics:  
C; Gene: ylfH  
C; Superfamily: nagD protein

Query Match 62.1%; Score 36; DB 2; Length 257;  
Best Local Similarity 87.5%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NTLKTPRV 8  
Db 47 NTLKTPRV 54

## RESULT 6

H86407  
F349.15 protein - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Nov-2001  
C:Accession: H86407  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marshall,  
R.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MID:21016719; PMID:11130712  
A:Accession: H86407  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <STO>  
A:Cross-references: GB:AE005172; NID:g9795618; PIDN:AAF98436.1; GSPDB:GN00141  
C:Genetics:  
A:Map\_position: 1

Query Match 62.1%; Score 36; DB 2; Length 266;  
Best Local Similarity 77.8%; Pred. No. 25;  
Matches 7; Conservative 1; Mismatches 1; Indels

```

Qy      2 TLKTPRVGG 10
        |||||: ||
Db     115 TLKTPQNGG 123

```

## RESULT 7

A64310  
methyl coenzyme M reductase (EC 1.8.-.-) II beta chain - Methanococcus jannaschii  
C/Species: Methanococcus jannaschii  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Apr-1999  
C/Accession: A64310  
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
E.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A;Reference number: A64300; MUID:96337999; PMID:8680807  
A;Accession: A64310  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-451 <BUL>  
A;Cross-references: GB:067465; GB:L77117; NID:gl590864; PID:gl590864; TIGR:MJ0081; PI  
C;Genetics:  
A;Map position: FOR74658-76013  
A;Start codon: TTG  
C;Superfamily: methyl coenzyme M reductase beta chain  
C;Keywords: methanogenesis; oxidoreductase

Query Match 62.1%; Score 36; DB 2; Length 451;  
Best Local Similarity 66.7%; Pred. No. 43;  
Matches 8; Conservative 0; Mismatches 4; Indels

Qy	1	NTLKT	PRVGGXA	12
Db	59	NALKT	GAVGGKA	70

## RESULT 8

E90853  
hypothetical protein ECs0197 [imported] - Escherichia coli (strain O157:H7, substrain  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C;Accession: E90653  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
gasawara, N.; Yasunaga, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g  
A;Reference numbers: A99629; MUID:21156231; PMID:11258796  
A;Accession: E90653  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-235 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA83620.1; PID:gl3359653; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECs0197

```
Query Match      60.3%; Score 35; DB 2; Length 235;
Best Local Similarity 54.5%; Pred. NO. 35;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 TLKTPRVGGXA 12  
|::|:|:|  
Db 74 TVRPPRLGGNA 84

RESULT 9

E85304  
 hypothetical protein 20207 [imported] - *Escherichia coli* (strain O157:H7, substrain E85304)  
 C/Species: *Escherichia coli*  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C/Accession: E85504  
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 iller, L.; Grotback, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
 Nature 409, 529-533, 2001  
 A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A/Reference number: A85480; PMID:21074935; PMID:11206551

A: Status: preliminary

A: Molecule type: DNA

A;ResIdues: 1-235 <STO>

A; Cross-references: GB:AE05174; NID:gl251226; PIDN:AAG54497.1; GSPDB:GN00145; UWG:  
A; Experimental source: strain O157:H7, substrain EDL933  
C; Genetics:  
A; Gene: Z0207

### Query Match

Query Match	00.3%	Score 35;	DB 2;	Length 235
Best Local Similarity	54.5%	Pred. No. 35;		
Matches	6:	Conservative	3:	Mismatches
			2:	Indels

QY 2 TLKTPRVGGXA 12  
I::|::|::|  
Db 74 TVRPPRLGGNA 84

## RESULT 10

C64744  
A:Species: *Escherichia coli* (strain K-12)  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: C64744  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
A:Title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: C64744  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-235 <BLAT>  
A:Cross-references: GB:AE000128; GB:U00096; MUID:g1786383; PIDN:AAC73306.1; PID:g1786393;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: yaeB

Query Match 60.3%; Score 35; DB 2; Length 235;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLKTPRVGGXA 12  
I::|::|::|  
Db 74 TVRPPRLGGNA 84

## RESULT 11

AG0532  
A:Title: conserved hypothetical protein STY0270 [imported] - *Salmonella enterica* subsp. *enterica*  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
A:Note: this species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AG0532  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
A:Title: Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AG0532  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-235 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD08703.1; PID:g16501526; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY0270

Query Match 60.3%; Score 35; DB 2; Length 235;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLKTPRVGGXA 12  
I::|::|::|  
Db 74 TVRPPRLGGNA 84

## RESULT 12

T34260  
A:Title: hypothetical protein F38E1.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T34260  
R:Gattung, S.; Le, T.

submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of *C. elegans* cosmid F38E1.

A:Reference number: Z21495  
A:Accession: T34260  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-310 <GAT>  
A:Cross-references: EMBL:U41996; PIDN:AAA83477.1; CESP:F38E1.3  
C:Genetics:  
A:Gene: CESP:F38E1.3  
A:Introns: 14/3; 69/3; 120/3; 166/3; 255/3; 294/3  
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 60.3%; Score 35; DB 2; Length 310;  
Best Local Similarity 87.5%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLKTPRV 8  
I::|::|::|  
Db 183 NKLATPRV 190

## RESULT 13

F83783  
A:Title: tartrate dehydrogenase BH1070 [imported] - *Bacillus halodurans* (strain C-125)  
C:Species: *Bacillus halodurans*  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: F83783  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fujii, F.; H. Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: F83783  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-353 <STO>  
A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04789.1; GSPDB:G  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1070  
C:Superfamily: 3-isopropylmalate dehydrogenase

Query Match 60.3%; Score 35; DB 2; Length 353;  
Best Local Similarity 60.0%; Pred. No. 53;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LKTPRVGGXA 12  
I::|::|::|  
Db 327 IKTPDIGRA 336

## RESULT 14

H70346  
A:Title: undecaprenyl-phosphate-alpha-N- acetylglucosaminyltransferase - *Aquifex aeolicus*  
C:Species: *Aquifex aeolicus*  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 03-Feb-2003  
C:Accession: H70346  
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V. Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: H70346  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-357 <AOF>  
A:Cross-references: GB:AE000694; NID:g2983162; PIDN:AAC06768.1; PID:g2983167; GB:AE00  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: rfe

Query Match 60.3%; Score 35; DB 2; Length 357;  
Best Local Similarity 75.0%; Pred. No. 54;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 TPRVGGXA 12  
|||:|:|  
Db 42 TPRIGGLA 49

## RESULT 15

## DEECPG

Phosphoglycerate dehydrogenase (EC 1.1.1.95) - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 01-Mar-2002

C:Accession: A25200; B38156; S22096; H65075

R:Tobey, K.L.; Grant, G.A.

J. Biol. Chem. 261, 12179-12183, 1986

A:Title: The nucleotide sequence of the serA gene of Escherichia coli and the amino acid

A:Reference number: A25200; MUID:86304370; PMID:3017965

A:Accession: A25200

A:Molecule type: DNA

A:Residues: 1-410 <TOB>

A:Cross-references: GB:L29397; GB:N00029; NID:g459754; PIDN:AAA24625.1; PID:g459755

R:Rex, J.H.; Aronson, B.D.; Somerville, R.L.

J. Bacteriol. 173, 5944-5953, 1991

A:Title: The tdh and serA operons of Escherichia coli: mutational analysis of the regula

A:Reference number: A38156; MUID:92011350; PMID:1917830

A:Accession: B38156

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-29 <REX>

A:Cross-references: GB:M64630; NID:g147807; PIDN:AAA73016.1; PID:g551837

R:Roy, I.; Leadlay, P.F.

submitted to the EMBL Data Library, June 1992

A:Reference number: S22096

A:Accession: S22096

A:Molecule type: DNA

A:Residues: 1-99 <ROY>

A:Cross-references: EMBL:X66836; NID:g42941; PIDN:CAA47308.1; PID:g42942

A:Experimental source: strain K12-38

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H65075

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-410 <BLAT>

A:Cross-references: GB:AR000374; GB:U00096; NID:g1789270; PIDN:AAAC75950.1; PID:g1789279;

A:Experimental source: strain K-12, substrain MG1635

C:Comment: The active enzyme is a tetramer of identical chains; it catalyzes the first c

oglyceric acid to 3-phosphohydroxypyruvic acid. In bacteria, this enzyme displays feedba

C:Genetics:

A:Gene: serA

A:Map position: 63 min

C:Superfamily: phosphoglycerate dehydrogenase

C:Keywords: NAD; oxidoreductase; serine biosynthesis

F:153-181/Region: beta-alpha-beta NAD nucleotide-binding fold

Query Match 60.3%; Score 35; DB 1; Length 410;

Best Local Similarity 60.0%; Pred. No. 61;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTLKTPRVGG 10

|||:|:|

Db 286 NVLLTPHIGG 295

Search completed: August 28, 2003, 18:39:06

Job time : 13.2727 secs